

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/404,832DATE: 04/05/95
TIME: 10:08:49

INPUT SET: S3120.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: DIXIT, VISHA M.

(ii) TITLE OF INVENTION: CD40 BINDING COMPOSITIONS AND METHODS OF
USING SAME

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER

(B) STREET: 755 Page Mill Road

(C) CITY: Palo Alto

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: KONSKI, ANTOINETTE F.

(B) REGISTRATION NUMBER: 34,202

(C) REFERENCE/DOCKET NUMBER: 203442102500

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 813-5600

(B) TELEFAX: (415) 494-0792

(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2339 base pairs

(B) TYPE: nucleic acid

ENTERED

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/404,832

DATE: 04/05/95
TIME: 10:08:54

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47      (C) STRANDEDNESS: single
48      (D) TOPOLOGY: linear
49
50
51
52      (ix) FEATURE:
53          (A) NAME/KEY: CDS
54          (B) LOCATION: 211..1911
55
56
57      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59      ACGAAGGCCA CGCGCCCGGC GCCCCTGAGC CGGCCGAGCG GCGACGGACC GCGAGATGAG      60
60
61      GAAAATGAGG CCCAAAGAAG TGATGCCACT TGGTTAAGGT CCCAGAGCAG GTCAGAATCA      120
62
63      GACCTAGGAT CAGAAACCTG GCTCCTGGCT CCTGCTCCCT ACTCTTCTAA GGATCGCTGT      180
64
65      CCTGACAGAA GAGAACTCCT CTTTCCTAAA ATG GAG TCG AGT AAA AAG ATG GAC      234
66      Met Glu Ser Ser Lys Lys Met Asp
67      1 5
68
69      TCT CCT GGC GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG CAC ACT GAC      282
70      Ser Pro Gly Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp
71      10 15 20
72
73      CGC AGT GCT GGG ACG CCA GTT TTT GTC CCT GAA CAA GGA GGT TAC AAG      330
74      Arg Ser Ala Gly Thr Pro Val Phe Val Pro Glu Gln Gly Gly Tyr Lys
75      25 30 35 40
76
77      GAA AAG TTT GTG AAG ACC GTG GAG GAC AAG TAC AAG TGT GAG AAG TGC      378
78      Glu Lys Phe Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu Lys Cys
79      45 50 55
80
81      CAC CTG GTG CTG TGC AGC CCG AAG CAG ACC GAG TGT GGG CAC CGC TTC      426
82      His Leu Val Leu Cys Ser Pro Lys Gln Thr Glu Cys Gly His Arg Phe
83      60 65 70
84
85      TGC GAG AGC TGC ATG GCG GCC CTG CTG AGC TCT TCA AGT CCA AAA TGT      474
86      Cys Glu Ser Cys Met Ala Ala Leu Leu Ser Ser Ser Ser Pro Lys Cys
87      75 80 85
88
89      ACA GCG TGT CAA GAG AGC ATC GTT AAA GAT AAG GTG TTT AAG GAT AAT      522
90      Thr Ala Cys Gln Glu Ser Ile Val Lys Asp Lys Val Phe Lys Asp Asn
91      90 95 100
92
93      TGC TGC AAG AGA GAA ATT CTG GCT CTT CAG ATC TAT TGT CGG AAT GAA      570
94      Cys Cys Lys Arg Glu Ile Leu Ala Leu Gln Ile Tyr Cys Arg Asn Glu
95      105 110 115 120
96
97      AGC AGA GGT TGT GCA GAG CAG TTA ATG CTG GGA CAT CTG GTG CAT TTA      618
98      Ser Arg Gly Cys Ala Glu Gln Leu Met Leu Gly His Leu Val His Leu
99      125 130 135

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100																		
101	AAA	AAT	GAT	TGC	CAT	TTT	GAA	GAA	CTT	CCA	TGT	GTG	CGT	CCT	GAC	TGC		666
102	Lys	Asn	Asp	Cys	His	Phe	Glu	Glu	Leu	Pro	Cys	Val	Arg	Pro	Asp	Cys		
103				140					145					150				
104																		
105	AAA	GAA	AAG	GTC	TTG	AGG	AAA	GAC	CTG	CGA	GAC	CAC	GTG	GAG	AAG	GCG		714
106	Lys	Glu	Lys	Val	Leu	Arg	Lys	Asp	Leu	Arg	Asp	His	Val	Glu	Lys	Ala		
107			155					160					165					
108																		
109	TGT	AAA	TAC	CGG	GAA	GCC	ACA	TGC	AGC	CAC	TGC	AAG	AGT	CAG	GTT	CCG		762
110	Cys	Lys	Tyr	Arg	Glu	Ala	Thr	Cys	Ser	His	Cys	Lys	Ser	Gln	Val	Pro		
111		170					175					180						
112																		
113	ATG	ATC	GCG	CTG	CAG	AAA	CAC	GAA	GAC	ACC	GAC	TGT	CCC	TGC	GTG	GTG		810
114	Met	Ile	Ala	Leu	Gln	Lys	His	Glu	Asp	Thr	Asp	Cys	Pro	Cys	Val	Val		
115	185					190					195					200		
116																		
117	GTG	TCC	TGC	CCT	CAC	AAG	TGC	AGC	GTC	CAG	ACT	CTC	CTG	AGG	AGC	GAG		858
118	Val	Ser	Cys	Pro	His	Lys	Cys	Ser	Val	Gln	Thr	Leu	Leu	Arg	Ser	Glu		
119					205					210					215			
120																		
121	TTG	AGT	GCA	CAC	TTG	TCA	GAG	TGT	GTC	AAT	GCC	CCC	AGC	ACC	TGT	AGT		906
122	Leu	Ser	Ala	His	Leu	Ser	Glu	Cys	Val	Asn	Ala	Pro	Ser	Thr	Cys	Ser		
123				220					225					230				
124																		
125	TTT	AAG	CGC	TAT	GGC	TGC	GTT	TTT	CAG	GGG	ACA	AAC	CAG	CAG	ATC	AAG		954
126	Phe	Lys	Arg	Tyr	Gly	Cys	Val	Phe	Gln	Gly	Thr	Asn	Gln	Gln	Ile	Lys		
127			235					240					245					
128																		
129	GCC	CAC	GAG	GCC	AGC	TCC	GCC	GTG	CAG	CAC	GTC	AAC	CTG	CTG	AAG	GAG		1002
130	Ala	His	Glu	Ala	Ser	Ser	Ala	Val	Gln	His	Val	Asn	Leu	Leu	Lys	Glu		
131		250					255					260						
132																		
133	TGG	AGC	AAC	TCG	CTC	GAA	AAG	AAG	GTT	TCC	TTG	TTG	CAG	AAT	GAA	AGT		1050
134	Trp	Ser	Asn	Ser	Leu	Glu	Lys	Lys	Val	Ser	Leu	Leu	Gln	Asn	Glu	Ser		
135	265					270					275					280		
136																		
137	GTA	GAA	AAA	AAC	AAG	AGC	ATA	CAA	AGT	TTG	CAC	AAT	CAG	ATA	TGT	AGC		1098
138	Val	Glu	Lys	Asn	Lys	Ser	Ile											

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153	GAA GCA GAC AGC ATG AAG AGC AGC GTG GAG TCC CTC CAG AAC CGC GTG	1290
154	Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val	
155	345 350 355 360	
156		
157	ACC GAG CTG GAG AGC GTG GAC AAG AGC GCG GGG CAA GTG GCT CGG AAC	1338
158	Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn	
159	365 370 375	
160		
161	ACA GGC CTG CTG GAG TCC CAG CTG AGC CGG CAT GAC CAG ATG CTG AGT	1386
162	Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser	
163	380 385 390	
164		
165	GTG CAC GAC ATC CGC CTA GCC GAC ATG GAC CTG GGC TTC CAG GTC CTG	1434
166	Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Gly Phe Gln Val Leu	
167	395 400 405	
168		
169	GAG ACC GCC AGC TAC AAT GGA GTG CTC ATC TGG AAG ATT CGC GAC TAC	1482
170	Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr	
171	410 415 420	
172		
173	AAG CGG CGG AAG CAG GAG GCC GTC ATG GGG AAG ACC CTG TCC CTT TAC	1530
174	Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr	
175	425 430 435 440	
176		
177	AGC CAG CCT TTC TAC ACT GGT TAC TTT GGC TAT AAG ATG TGT GCC AGG	1578
178	Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg	
179	445 450 455	
180		
181	GTC TAC CTG AAC GGG GAC GGG ATG GGG AAG GGG ACG CAC TTG TCG CTG	1626
182	Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu	
183	460 465 470	
184		
185	TTT TTT GTC ATC ATG CGT GGA GAA TAT GAT GCC CTG CTT CCT TGG CCG	1674
186	Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro	
187	475 480 485	
188		
189	TTT AAG CAG AAA GTG ACA CTC ATG CTG ATG GAT CAG GGG TCC TCT CGA	1722
190	Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg	
191	490 495 500	
192		
193	CGT CAT TTG GGA GAT GCA TTC AAG CCC GAC CCC AAC AGC AGC AGC TTC	1770
194	Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe	
195	505 510 515 520	
196		
197	AAG AAG CCC ACT GGA GAG ATG AAT ATC GCC TCT GGC TGC CCA GTC TTT	1818
198	Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe	
199	525 530 535	
200		
201	GTG GCC CAA ACT GTT CTA GAA AAT GGG ACA TAT ATT AAA GAT GAT ACA	1866
202	Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr	
203	540 545 550	
204		
205	ATT TTT ATT AAA GTC ATA GTG GAT ACT TCG GAT CTG CCC GAT CCC	1911

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206   Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
207           555                      560                      565
208
209   TGATAAGTAG CTGGGGAGGT GGATTTAGCA GAAGGCAACT CCTCTGGGGG ATTTGAACCG      1971
210
211   GTCTGTCTTC ACTGAGGTCC TCGCGCTCAG AAAAGGACCT TGTGAGACGG AGGAAGCGGC      2031
212
213   AGAAGGCGGA CGCGTGCCGG CGGGAGGAGC CACGCGAGAG CACACCTGAC ACGTTTTATA      2091
214
215   ATAGACTAGC CACACTTCAC TCTGAAGAAT TATTTATCCT TCAACAAGAT AAATATTGCT      2151
216
217   GTCAGAGAAG GTTTTCATTT TCATTTTAA AGATCTAGTT AATTAAGGTG GAAAACATAT      2211
218
219   ATGCTAAACA AAAGAAACAT GATTTTCTT CCTTAACTT GAACACCAA AAAACACACA      2271
220
221   CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT AAGTAAAAGG AGAATTTATG      2331
222
223   AAATAGTA                                     2339
224
225

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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237   Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
238       1              5              10              15
239
240   Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
241           20              25              30
242
243   Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
244           35              40              45
245
246   Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
247           50              55              60
248
249   Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
250           65              70              75              80
251
252   Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
253           85              90              95
254
255   Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
256           100             105             110
257
258   Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/404,832

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Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: US